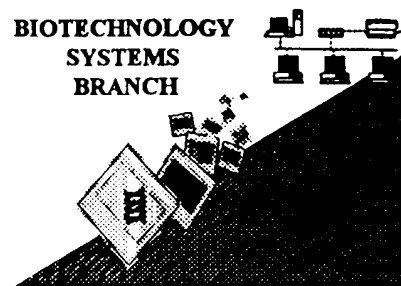


RAW SEQUENCE LISTING

ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/403,980
Art Unit / Team No. : BATCH 1615-3/17
Date Processed by STIC: 4/13/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/403,980

BATCH

DATE: 04/13/2000
TIME: 13:47:38

Input Set: I403980.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: I.N.S.E.R.M.
2 <120> TITLE OF INVENTION: NEW POLYPEPTIDES ASSOCIATED WITH ACTIVATORY RECEPTORS
3 AND THEIR BIOLOGICAL APPLICATIONS
4 <130> FILE REFERENCE: PCT/FR98/00883
5 <140> CURRENT APPLICATION NUMBER: US/09/403,980
6 <141> CURRENT FILING DATE: 2000-01-19
7 <150> EARLIER APPLICATION NUMBER: FR97/05411
8 <151> EARLIER FILING DATE: 1997-04-30
9 <160> NUMBER OF SEQ ID NOS: 31
10 <170> SOFTWARE: PatentIn Ver. 2.1
11 <210> SEQ ID NO 1
12 <211> LENGTH: 517
13 <212> TYPE: DNA
14 <213> ORGANISM: Mus musculus
15 <400> SEQUENCE: 1
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17 ggggctctgg agcctcctgg tgccttctgt tccttctgt cctcctgact gtgggaggat 120
18 taagtcccgat acaggcccag agtgacactt tcccaagatg cgactgttct tccgtgagcc 180
19 ctggtgtact gtctgggatt gttctgggtg acttggtgtt gactctgtg attgccctgg 240
20 ctgtgtactc tctgggccgc ctggtctccc gaggtcaagg gacagcggaa gggaccggga 300
21 aacaacacat tgctgagact gattgcctcc atcaggagct tcagggtcag agacatgaag 360
22 tatacagtga cctcaacaca cagaggcaat attacagatg agcccactct atgccatca 420
23 gcggcctgat gcccgatcc ggtcattcca gatgcctact caacaagccc tctctgagat 480
24 caggactccc gttggaatac agatccacag ggtaccc 517
25 <210> SEQ ID NO 2
26 <211> LENGTH: 87
27 <212> TYPE: PRT
28 <213> ORGANISM: Mus musculus
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31 1 5 10 15
32 Val Leu Ser Gly Ile Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile
33 20 25 30
34 Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly
35 35 40 45
36 Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro
37 50 55 60
38 Tyr Gln Glu Leu Gln Gly Gln Arg His Glu Val Tyr Ser Asp Leu Asn
39 65 70 75 80
40 Thr Gln Arg Gln Tyr Tyr Arg 85
41
42 <210> SEQ ID NO 3
43 <211> LENGTH: 16
44 <212> TYPE: PRT

RAW SEQUENCE LISTING
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45 <213> ORGANISM: Mus musculus
46 <400> SEQUENCE: 3
47 Gln Ser Asp Thr Phe Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly
48 1 5 10 15
49 <210> SEQ ID NO 4
50 <211> LENGTH: 24
51 <212> TYPE: PRT
52 <213> ORGANISM: Mus musculus
53 <400> SEQUENCE: 4
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55 1 5 10 15
56 Ala Leu Ala Val Tyr Ser Leu Gly
57 20
58 <210> SEQ ID NO 5
59 <211> LENGTH: 47
60 <212> TYPE: PRT
61 <213> ORGANISM: Mus musculus
62 <400> SEQUENCE: 5
63 Arg Leu Val Ser Arg Gly Gln Gly Thr Ala Glu Gly Thr Arg Lys Gln
64 1 5 10 15
65 His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg
66 20 25 30
67 His Glu Val Tyr Ser Asp Leu Asn Thr Gln Arg Gln Tyr Tyr Arg
68 35 40 45
69 <210> SEQ ID NO 6
70 <211> LENGTH: 515
71 <212> TYPE: DNA
72 <213> ORGANISM: Mus musculus
73 <400> SEQUENCE: 6
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75 ggctctggag cctcctgggtg ccttctgttc cttcctgtcc tctgactgt gggaggatta 120
76 agtcccgtac aggccagag tgacactttc ccaagatgcg actgttcttc cgtgagccct 180
77 ggtgtactgt ctgggattgt tctgggtgac ttggtgttga ctctgctgat tgccctggct 240
78 gtgtactctc tgggcccgtt ggtctcccga ggtcaaggga cagcggaagg gacccggaaa 300
79 caacacattg ctgagactga gtcgccttat caggagcttc agggtcagag acatgaagta 360
80 tacagtgacc tcaacacaca gaggcaatat tacagatgag cccactctat gccatcagc 420
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82 ggactcccgt tggaatacac atccacaggg tacct 515
83 <210> SEQ ID NO 7
84 <211> LENGTH: 371
85 <212> TYPE: DNA
86 <213> ORGANISM: Mus musculus
87 <400> SEQUENCE: 7
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89 tctcctgac tggggaggga ttaagtcccg tacaggccca gactgacact ttcccaagat 120
90 ggcactgttc ttccgtgagc cctgggtgtac tggctgggat tgttctgggt gacttggtgt 180
91 tgactctgct gattgccctg gctgtgtact ctctcgccg cctgggtctcc cgaggtaag 240
92 ggacagcga agggacccgg aaacaacaca ttgctgagac tgagtcgctt tatcaggagc 300
93 ttcagggtca gagaccagaa gtatacagt acctcaacac acagaggcaa tattacagat 360
94 gagccactc t 371

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/403,980

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96 <211> LENGTH: 376
97 <212> TYPE: DNA
98 <213> ORGANISM: Mus musculus
99 <400> SEQUENCE: 8
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101 gtgacacttt cccaagatgc ggctgttctt ccgtgagccc tgggtgactg gctgggattg 120
102 ttctgggtga cttgggtgtg actctgctga ttgccctggc tgtgtactct ctgggccgcc 180
103 tggctctccg aggtcaaggg acagcggaag ggaccggaa acaacacatt gctgagactg 240
104 agtcgcctta tcaggagctt cagggtcaga gacatgaagt atacagtac ctcaacacac 300
105 agaggcaata ttacagatga gccactcta tgcccatcag cggcctgatg cccggatccg 360
106 gtcattccag atgctt                                     376
107 <210> SEQ ID NO 9
108 <211> LENGTH: 402
109 <212> TYPE: DNA
110 <213> ORGANISM: Mus musculus
111 <400> SEQUENCE: 9
112 ccagcccctg gactgtggtg tccagtgcac atctggccac catgggggct ctggagcctc 60
113 ctgggtgcctt ctgttccttc ctgtcctcct gactgtggga ggattaagtc ccgtacaggc 120
114 ccagagtgcac actttcccaa gatgcgactg ttcttcctg agccctgggt tactggctgg 180
115 gattgttctg ggtgacttgg tgttgactct gctgattgcc ctggctgtgt actctctggg 240
116 ccgcctggtc tcccagagtc aagggaacgc ggaagggacc cggaacaac acattgctga 300
117 gactgagtcg ccttatcagg agcttcaggg tcagagacca gaagtataca gtgacctcaa 360
118 cacacagagg caatattaca gatgagccac tctatgcca tc                                     402
119 <210> SEQ ID NO 10
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121 <212> TYPE: DNA
122 <213> ORGANISM: Mus musculus
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124 gttccttctt gtcctcctga ctgtgggagg attaagtccc gtacaggccc agagtgcac 60
125 tttcccaaga tgcgactgtt cttccgtgag ccctgggtga ctggctggga ttgttctggg 120
126 tgacttggtg ttgactctgc tgattgcctt ggctgtgtac tctctgggcc gcttggtctc 180
127 ccgaggtcaa gggacagcgg aagggaaccc gaaacaacac attgctgaga ctgagtcgcc 240
128 ttatcaggag cttcagggtc agagacctga agtatacagt gacctcaaca cacagaggcg 300
129 atattacaga tgagccact ctatgcccat cagcggcctg atgcccggat ccggtcattc 360
130 cagatgccta ctcaacaagc cttctgtggt gatcaggact cccgttggaa tacagatcca 420
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133 <210> SEQ ID NO 11
134 <211> LENGTH: 171
135 <212> TYPE: PRT
136 <213> ORGANISM: Mus musculus
137 <400> SEQUENCE: 11
138 Ser His Gln Val Pro Pro Ala Pro Gly Leu Trp Cys Pro Val His Ile
139      1          5          10          15
140 Trp Pro Pro Trp Gly Ser Gly Ala Ser Trp Cys Leu Leu Phe Leu Pro
141          20          25          30
142 Val Leu Leu Thr Val Gly Gly Leu Ser Pro Val Gln Ala Gln Ser Asp
143          35          40          45
144 Thr Phe Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly Val Leu Ser

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145 50 55 60
146 Gly Ile Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile Ala Leu Ala 80
147 65 70 75
148 Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly Thr Ala Glu 95
149 85 90
150 Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu 110
151 100 105
152 Leu Gln Gly Gln Arg His Glu Val Tyr Ser Asp Leu Asn Thr Gln Arg 125
153 115 120
154 Gln Tyr Tyr Arg **Xaa** Ala His Ser Met Pro Ile Ser Gly Leu Met Pro 140
155 130 135
156 Gly Ser Gly His Ser Arg Cys Leu Leu Asn Lys Pro Ser Leu Arg Ser 160
157 145 150 155
158 Gly Leu Pro Leu Glu Tyr Arg Ser Thr Gly Tyr 170
159 165
160 <210> SEQ ID NO 12
161 <211> LENGTH: 123
162 <212> TYPE: PRT
163 <213> ORGANISM: Mus musculus
164 <400> SEQUENCE: 12
165 Ala Tyr Leu Ala Thr Met Gly Ala Leu Glu Pro Pro Trp Cys Leu Leu 15
166 1 5 10
167 Phe Leu Pro Val Leu Leu Thr Val Gly Gly Leu Ser Pro Val Gln Ala 30
168 20 25
169 Gln Ser Asp Thr Phe Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly 45
170 35 40
171 Val Leu Ala Gly Ile Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile 60
172 50 55
173 Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly 80
174 65 70 75
175 Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro 95
176 85 90
177 Tyr Gln Glu Leu Gln Gly Gln Arg Pro Glu Val Tyr Ser Asp Leu Asn 110
178 100 105
179 Thr Gln Arg Gln Tyr Tyr Arg **Xaa** Ala His Ser 120
180 115
181 <210> SEQ ID NO 13
182 <211> LENGTH: 124
183 <212> TYPE: PRT
184 <213> ORGANISM: Mus musculus
185 <400> SEQUENCE: 13
186 Leu Leu Phe Leu Pro Val Leu Leu Thr Val Gly Gly Leu Ser Pro Val 15
187 1 5 10
188 Gln Ala Gln Ser Asp Thr Phe Pro Arg Cys Gly Cys Ser Ser Val Ser 30
189 20 25
190 Pro Gly Val Leu Ala Gly Ile Val Leu Gly Asp Leu Val Leu Thr Leu 45
191 35 40
192 Leu Ile Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly 60
193 50 55
194 Gln Gly Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu

W-->

W-->

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195 65 70 75 80
 196 Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg His Glu Val Tyr Ser Asp
 197 85 90 95
 W--> 198 *item 10* Leu Asn Thr Gln Arg Gln Tyr Tyr Arg Xaa Ala His Ser Met Pro Ile
 199 100 105 110
 200 Ser Gly Leu Met Pro Gly Ser Gly His Ser Arg Cys
 201 115 120
 202 <210> SEQ ID NO 14
 203 <211> LENGTH: 133
 204 <212> TYPE: PRT
 205 <213> ORGANISM: Mus musculus
 206 <400> SEQUENCE: 14
 207 Gln Pro Leu Asp Cys Gly Val Gln Cys Ile Ser Gly His His Gly Gly
 208 1 5 10 15
 209 Ser Gly Ala Ser Trp Cys Leu Leu Phe Leu Pro Val Leu Leu Thr Val
 210 20 25 30
 211 Gly Gly Leu Ser Pro Val Gln Ala Gln Ser Asp Thr Phe Pro Arg Cys
 212 35 40 45
 213 Asp Cys Ser Ser Val Ser Pro Gly Val Leu Ala Gly Ile Val Leu Gly
 214 50 55 60
 215 Asp Leu Val Leu Thr Leu Leu Ile Ala Leu Ala Val Tyr Ser Leu Gly
 216 65 70 75 80
 217 Arg Leu Val Ser Arg Gly Gln Gly Thr Ala Glu Gly Thr Arg Lys Gln
 218 85 90 95
 219 His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg
 220 100 105 110
 W--> 221 Pro Glu Val Tyr Ser Asp Leu Asn Thr Gln Arg Gln Tyr Tyr Arg Xaa *item 10*
 222 115 120 125
 223 Ala Thr Leu Cys Pro
 224 130
 225 <210> SEQ ID NO 15
 226 <211> LENGTH: 160
 227 <212> TYPE: PRT
 228 <213> ORGANISM: Mus musculus
 229 <400> SEQUENCE: 15
 230 Phe Leu Pro Val Leu Leu Thr Val Gly Gly Leu Ser Pro Val Gln Ala
 231 1 5 10 15
 232 Gln Ser Asp Thr Phe Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly
 233 20 25 30
 234 Val Leu Ala Gly Ile Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile
 235 35 40 45
 236 Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly
 237 50 55 60
 238 Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro
 239 65 70 75 80
 240 Tyr Gln Glu Leu Gln Gly Gln Arg Pro Glu Val Tyr Ser Asp Leu Asn
 241 85 90 95
 W--> 242 Thr Gln Arg Arg Tyr Tyr Arg Xaa Ala His Ser Met Pro Ile Ser Gly *item 10*
 243 100 105 110
 Leu Met Pro Gly Ser Gly His Ser Arg Cys Leu Leu Asn Lys Pro Phe

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
 Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
 <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION US/09/403,980DATE: 04/13/2000
TIME: 13:47:38

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Line	Error/Warning	Original Text
154	W "N" or "Xaa" used: Feature required	Gln Tyr Tyr Arg Xaa Ala His Ser Met Pro I
179	W "N" or "Xaa" used: Feature required	Thr Gln Arg Gln Tyr Tyr Arg Xaa Ala His S
198	W "N" or "Xaa" used: Feature required	Leu Asn Thr Gln Arg Gln Tyr Tyr Arg Xaa A
221	W "N" or "Xaa" used: Feature required	Pro Glu Val Tyr Ser Asp Leu Asn Thr Gln A
242	W "N" or "Xaa" used: Feature required	Thr Gln Arg Arg Tyr Tyr Arg Xaa Ala His S
248	W "N" or "Xaa" used: Feature required	Xaa Asp Ile Xaa His Cys Thr Ile Ser Val P
282	W "N" or "Xaa" used: Feature required	Ser Asp Leu Asn Thr Gln Arg Gln Tyr Tyr A

Raw Sequence Listing Error Summary

[illegible]

SERIAL NUMBER: 09/403980

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | | |
|----|-------|----------------------------------|--|
| 1 | _____ | Wrapped Nucleics | The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". |
| 2 | _____ | Wrapped Aminos | The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". |
| 3 | _____ | Incorrect Line Length | The rules require that a line not exceed 72 characters in length. This includes spaces. |
| 4 | _____ | Misaligned Amino Acid Numbering | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers. |
| 5 | _____ | Non-ASCII | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed. |
| 6 | _____ | Variable Length | Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. |
| 7 | _____ | PatentIn ver. 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. |
| 8 | _____ | Skipped Sequences (OLD RULES) | Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). |
| 9 | _____ | Skipped Sequences (NEW RULES) | Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 10 | _____ | Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa , and which residue n or Xaa represents. |
| 11 | _____ | Use of <213>Organism (NEW RULES) | Sequence(s) _____ are missing this mandatory field or its response. |
| 12 | _____ | Use of <220>Feature (NEW RULES) | Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules) |
| 13 | _____ | PatentIn ver. 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk. |